REMARKS

As noted in the Reply filed April 17, 2001, the sequence identification at page 19, lines 26-31 is correct. A peptide sequence having 20 residues, which begins D-D-D and ends H-H-H-, and which is written on two lines, is listed in the Sequence Listing as SEQ ID NO: 26. A nucleic acid sequence having 72 bases, which begins with GCGGCC and ends with TAG and which is written on two lines, is isted in the Sequence Listing as SEQ ID NO: 25.

With regard to the objection to the hyperlinks in the specification (presumably at page 15, lines 5-7), applicants have amended the specification so that there is no longer an active hyperlink to the internet. The change does not represent new matter, because it is merely a restatement of the disclosure which was originally present in the specification.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 15, line 1 to line 11 as follows:

Residues subject to random mutation are Vk CDR3 positions 91, 93, 94 and 96 (yellow), and VH CDR3 positions 95, 96, 97, and 98 (blue). The Cb atoms of these side chains are shown in darker colours. Also shown (in grey), are the residues of CDR1 and CDR2, which can be mutated to improve antibody affinity. Using the program RasMol, which can be found on the World Wide Web at ~~(http://www~~ chemistry.ucsc.edu/wipke/teaching/rasmol.html~~)~~, the structure of scFv were modeled from pdb file 1igm (Brookhaven Proten Data Bank; which can be found on the World Wide Web at ~~http://www2~~ ebi.ac.uk/pcserv/pdbdb.htm). (b) PCR amplification and library cloning strategy. The DP47 and DPK22 germline templates were modified (see text) to generate mutations in the CDR3 regions. Genes are indicated as rectangles, and CDRs as numbered boxes within the rectangle. The VH and the VL segments were then assembled and cloned in pDN332 phagemid vector.